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Title: DOE/NCI Pilot 2: Molecular Determinants of Cancer

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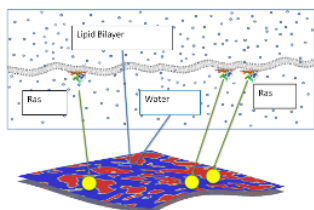
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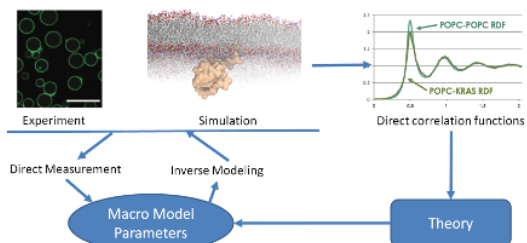
DOE/NCI Pilot 2: Molecular Determinants of Cancer

Aim 1: Spatial hierarchical multi-scale modeling

Coupled continuum and particle simulations



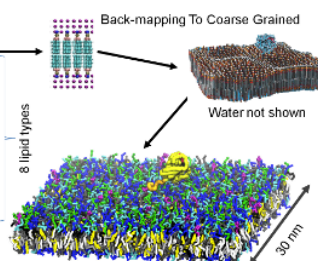
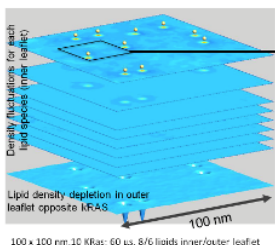
Macro-scale model is informed by experiment and simulation



Macro to micro scale coupling

Macro Scale: continuum Phase Field Model

Micro Scale: Coarse Grained Bead Martini Model



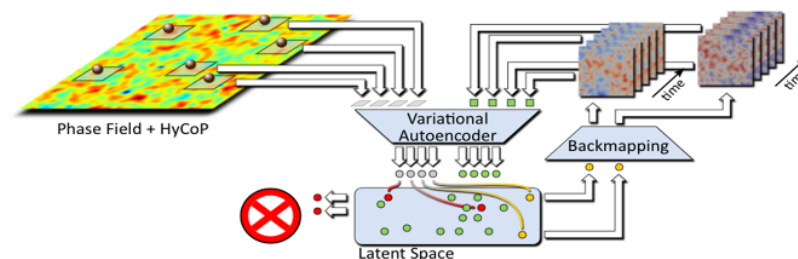
DOE

Novel multi-scale modeling framework allows investigation of continuum phenomenon informed by atomistic behavior.

NCI

Significantly enhance ability to perform predictive simulations on biologically relevant time and length scales

Aim 2: Machine-learning enabled dynamic validation approach to high-fidelity simulation



Steering multi-scale simulations by adaptively sampling data-driven latent spaces:

- (1) Train latent space representing space of relevant lipid configurations.
- (2) Dynamically sample configuration space to understand RAS-membrane interactions at macro time-scales with micro precision

DOE

Powerful ability to steer multiple large-scale simulations on next-generation computing, defining requirements for exascale

NCI

Combined experimental and simulation campaign of exploration leads to potential therapeutics for Ras-related cancers

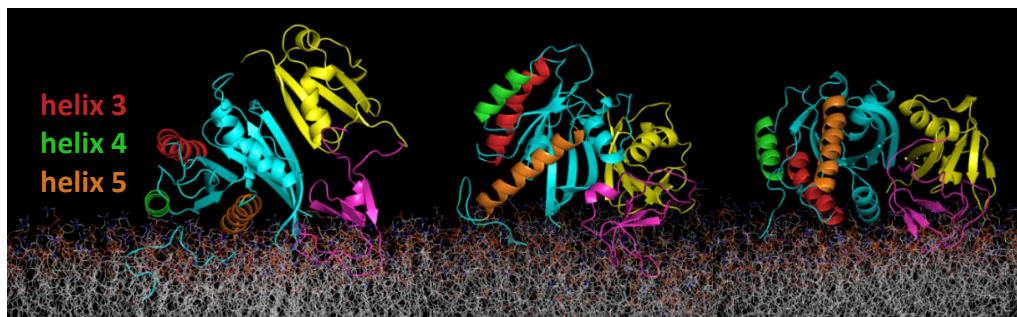
This work has been supported in part by the Joint Design of Advanced Computing Solutions for Cancer (JDACS4C) program established by the U.S. Department of Energy (DOE) and the National Cancer Institute (NCI) of the National Institutes of Health. This work was performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under Contract DE-AC52-07NA27344, Los Alamos National Laboratory under Contract DE-AC5206NA25396, Oak Ridge National Laboratory under Contract DE-AC05-00OR22725, and Frederick National Laboratory for Cancer Research under Contract HHSN261200800001E.



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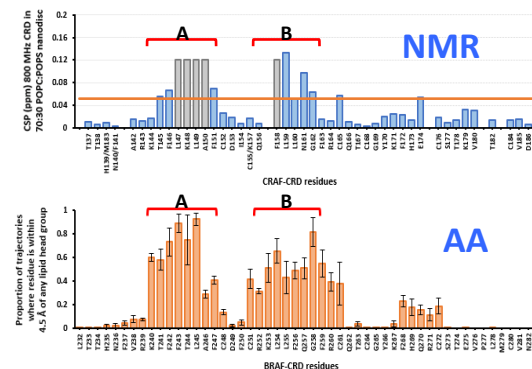
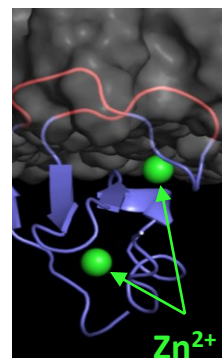
Resulting orientations:

Exposed

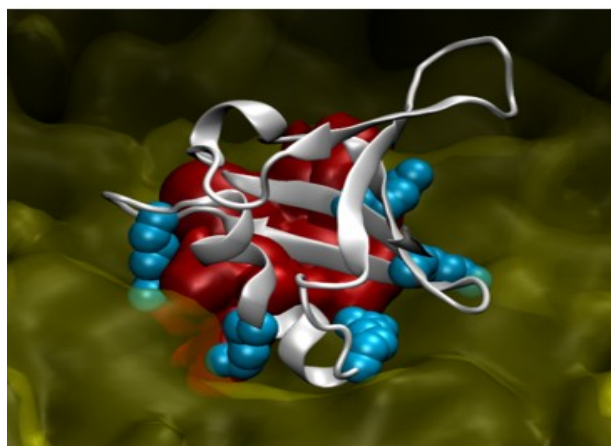
Membrane-adjacent/GH5

Membrane-adjacent/GH3

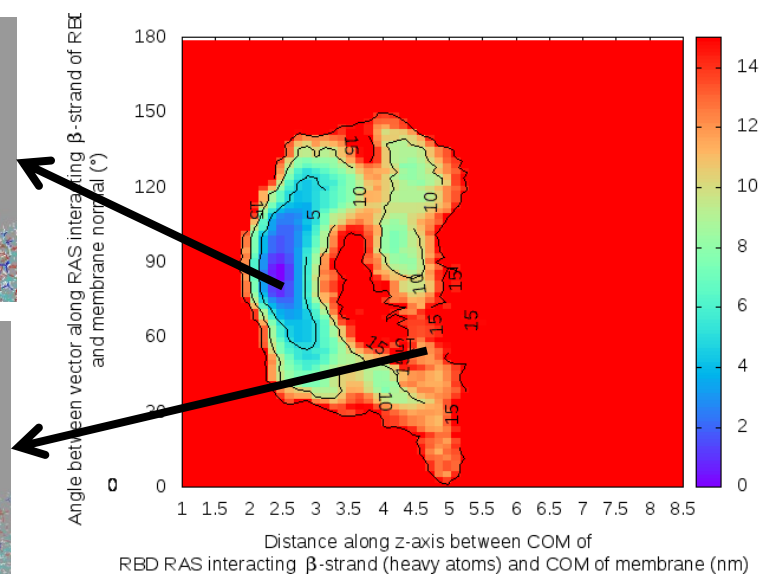
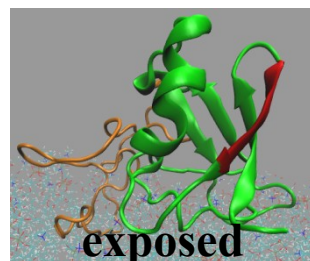
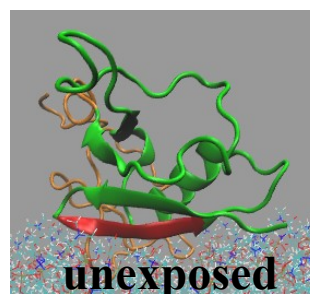
Membrane anchoring of RAF-CRD provides a basis for exploring models of membrane-associated KRAS/RAF-RBD/RAF-CRD ternary complex



(Left) Membrane anchoring of the CRAF CRD involves two hydrophobic loops. (Right) Lipid-protein contact profiles of CRD. Larger values indicate stronger membrane association.

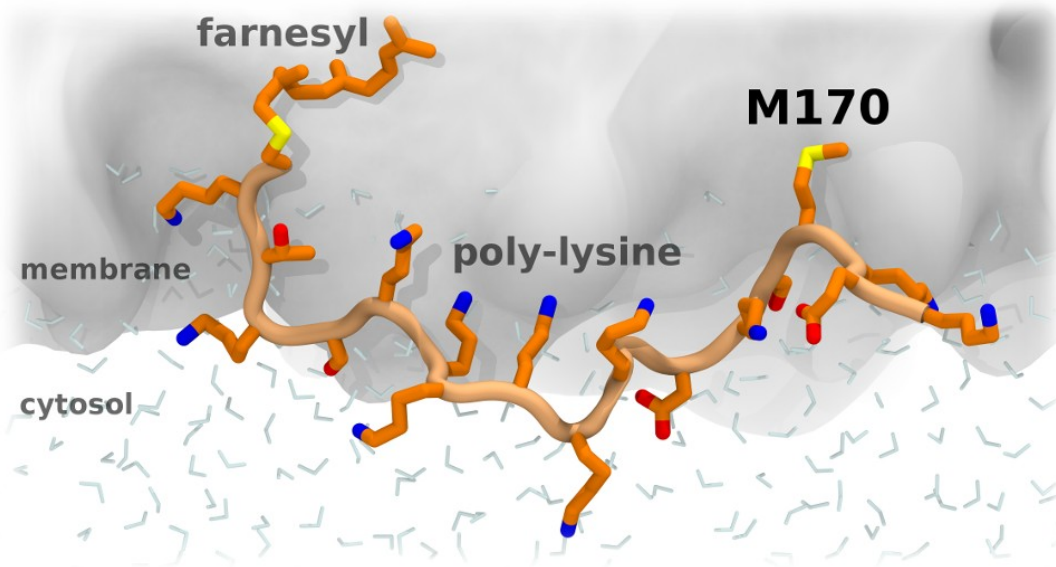


Weak binding of the RBD to a lipid membrane. Close contacts occur via the basic residues such as Lys and Arg (blue) of the RBD and PS lipids of the membrane. The binding of RBD is very weak due to the presence of a water layer (red) in between the RBD and membrane.

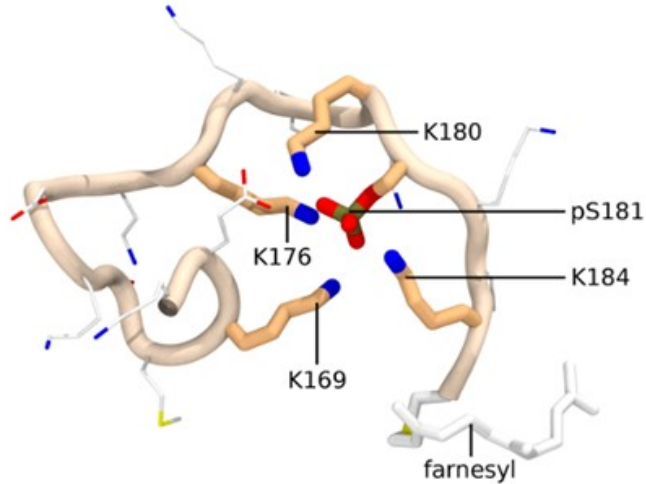


Free energy map showing the exposed and unexposed conformations adopted by the RBD, w.r.t. RAS. When the RBD is connected to the CRD, the RBD is able to explore more of the conformational space that could also lead to biologically important events.

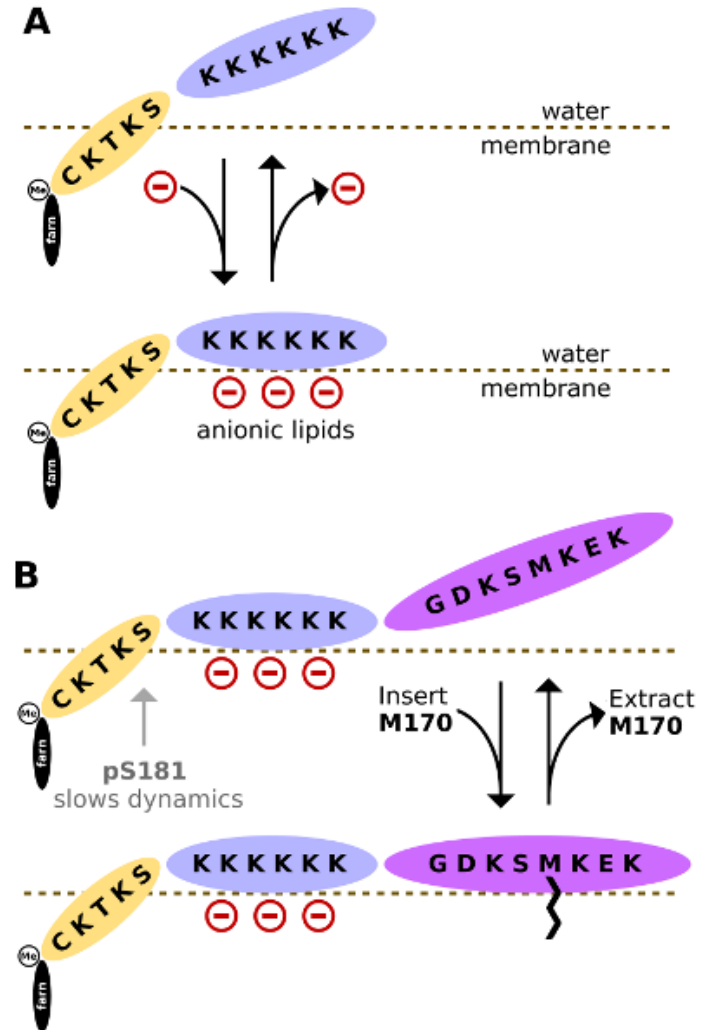
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Methionine 170 is a reversible membrane anchor



Regulatory phosphorylation slows the dynamics of this anchor



Proposed model by which lipids influence Ras' membrane tether